



**Supplementary information, Fig. S5 Analysis of the interface between cGAS site B and the bound nucleosome.** **a** Different conformations of the Loop 2 shown by superposition of the structures of the nucleosome bound cGAS (hot pink), the cGAS in apo state (PDB:4LEV, pink) and the cGAS in dsDNA binding state (PDB: 6CT9, wheat). **b** Potential contacts between residues from cGAS site B and the nucleosomal DNA. **c** The side chain of the cGAS R255 inserted to the acidic cavity of H2A shown as electrostatic surface representation. Red represents negative charge, and blue represents positive charge. **d-j** Comparison of the commonly binding mode of the arginine residues to the acidic cavity of H2A. **d** cGAS. **e** IE1 (PDB: 5E5A). **f** Sir3 (PDB: 4KUD). **g** LANA (PDB: 1ZLA). **h** PRC1 (PDB: 4R8P). **i** RCC1 (PDB: 3MVD). **j** CENP-C (4X23).